NCBI   ●●●●●●●●●●●●○○○ ○○○○ ●●●●●● **ⁱProtein**

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy

Search Protein ▼ for _____

Limits   Preview/Index   History   Clipboard

Display GenPept ▼ Save Text   Add to Clipboard

☐1: P02932. OUTER MEMBRANE   BLink, Related Sequences, PubMed,
PO...[gi:130121]   Taxonomy, LinkOut

```
LOCUS        PHOE_ECOLI     351 aa                            BCT
DEFINITION   OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
ACCESSION    P02932
PID          g130121
VERSION      P02932  GI:130121
DBSOURCE     swissprot: locus PHOE_ECOLI, accession P02932;
             class: standard.
             created: Jul 21, 1986.
             sequence updated: Jul 21, 1986.
             annotation updated: Aug 20, 2001.
             xrefs: gi: gi: 42389, gi: gi: 42391, gi: gi: 236
             1786436, gi: gi: 4902908, gi: gi: 4902976, gi: g
             1552809, gi: gi: 42495, gi: gi: 42496, gi: gi: 7
             443180
             xrefs (non-sequence databases): SWISS-2DPAGE P02
             B037.0, EcoGene EG10729, InterPro IPR001702, Pfa
             PR00182, PRINTS PR00183, PROSITE PS00576
KEYWORDS     Outer membrane; Transmembrane; Porin; Signal; 3D
             Complete proteome.
SOURCE       Escherichia coli.
  ORGANISM   Escherichia coli
             Bacteria; Proteobacteria; gamma subdivision; Ent
             Escherichia.
REFERENCE    1   (residues 1 to 351)
  AUTHORS    Overbeeke,N., Bergmans,H., van Mansfeld,F. and L
  TITLE      Complete nucleotide sequence of phoE, the struct
             phosphate limitation inducible outer membrane po
             Escherichia coli K12
  JOURNAL    J. Mol. Biol. 163 (4), 513-532 (1983)
  MEDLINE    83189086
  REMARK     SEQUENCE FROM N.A.
             STRAIN=K12
REFERENCE    2   (residues 1 to 351)
  AUTHORS    Blattner,F.R., Plunkett,G.I.I., Bloch,C.A., Pe
```

Burland,V., Riley,M., Collado-Vides,J., Glasner,
Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,
Rose,D.J., Mau,B. and Shao,Y.
TITLE   The complete genome sequence of Escherichia coli
JOURNAL   Science 277 (5331), 1453-1474 (1997)
MEDLINE   97426617
REMARK   SEQUENCE FROM N.A.
           STRAIN=K12 / MG1655
REFERENCE 3   (residues 1 to 351)
AUTHORS   Takemoto,K., Mori,H., Murayama,N., Kataoka,K., Y
           Yamamoto,Y., Inokuchi,H., Miki,T., Hatada,E., Fu
           Ichihara,S., Mizuno,T., Makino,K., Nakata,A., Yu
           and Mizobuchi,K.
TITLE   Direct Submission
JOURNAL   Submitted (??-FEB-1996)
REMARK   SEQUENCE FROM N.A.
           STRAIN=K12 / W3110
REFERENCE 4   (residues 1 to 351)
AUTHORS   Schramm,S., Duncan,M., Allen,E., Araujo,R., Apar
           Davis,K., Federspiel,N., Hyman,R., Kalman,S., Ko
           Lashkari,D., Lew,H., Lin,D., Namath,A., Oefner,P
           Davis,R.W.
TITLE   Direct Submission
JOURNAL   Submitted (??-SEP-1996)
REMARK   SEQUENCE FROM N.A.
REFERENCE 5   (residues 1 to 351)
AUTHORS   Deutch,A.H., Rushlow,K.E. and Smith,C.J.
TITLE   Analysis of the Escherichia coli proBA locus by
           sequencing
JOURNAL   Nucleic Acids Res. 12 (15), 6337-6355 (1984)
MEDLINE   84297232
REMARK   SEQUENCE OF 1-22 FROM N.A.
REFERENCE 6   (residues 1 to 351)
AUTHORS   Struyve,M., Moons,M. and Tommassen,J.
TITLE   Carboxy-terminal phenylalanine is essential for
           assembly of a bacterial outer membrane protein
JOURNAL   J. Mol. Biol. 218 (1), 141-148 (1991)
MEDLINE   91162638
REMARK   MUTAGENESIS OF PHE-351.
REFERENCE 7   (residues 1 to 351)
AUTHORS   Jap,B.K., Walian,P.J. and Gehring,K.
TITLE   Structural architecture of an outer membrane cha
           by electron crystallography
JOURNAL   Nature 350 (6314), 167-170 (1991)
MEDLINE   91172301
REMARK   X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).

```
REFERENCE      8   (residues 1 to 351)
  AUTHORS      Cowan,S.W., Schirmer,T., Rummel,G., Steiert,M.,
               Pauptit,R.A., Jansonius,J.N. and Rosenbusch,J.P.
  TITLE        Crystal structures explain functional properties
               porins
  JOURNAL      Nature 358 (6389), 727-733 (1992)
  MEDLINE      92375189
  REMARK       X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
REFERENCE      9   (residues 1 to 351)
  AUTHORS      Struyve,M., Visser,J., Adriaanse,H., Benz,R. and
  TITLE        Topology of PhoE porin: the 'eyelet' region
  JOURNAL      Mol. Microbiol. 7 (1), 131-140 (1993)
  MEDLINE      93172954
  REMARK       TOPOLOGY.
COMMENT                  -------------------------------------------------
               This SWISS-PROT entry is copyright. It is produc
               collaboration between the Swiss Institute of Bio
               the EMBL outstation - the European Bioinformatic
               The original entry is available from http://www.
               and http://www.ebi.ac.uk/sprot
                         -------------------------------------------------
               [FUNCTION] THIS IS ONE OF THE PROTEINS INDUCED W
               ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEI
               PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANI
               PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIV
               SOLUTES.
               [SUBUNIT] HOMOTRIMER.
               [SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN
               [SIMILARITY] BELONGS TO THE OMPC/PHOE FAMILY OF
FEATURES             Location/Qualifiers
     source          1..351
                     /organism="Escherichia coli"
                     /db_xref="taxon:562"
                     1..351
     Protein         1..351
                     /product="OUTER MEMBRANE PORE PROTEIN E
     Region          1..21
                     /region_name="Signal"
     Region          22..351
                     /region_name="Mature chain"
                     /note="OUTER MEMBRANE PORE PROTEIN E."
     Region          25..26
                     /region_name="Beta-strand region"
     Region          30..35
                     /region_name="Beta-strand region"
     Region          37..45
```

```
                            /region_name="Beta-strand region"
         Region             52..53
                            /region_name="Beta-strand region"
         Region             56..65
                            /region_name="Beta-strand region"
         Region             71..82
                            /region_name="Beta-strand region"
         Region             87..88
                            /region_name="Hydrogen bonded turn"
         Region             93..104
                            /region_name="Beta-strand region"
         Region             105..107
                            /region_name="Hydrogen bonded turn"
         Region             108..116
                            /region_name="Beta-strand region"
         Region             119
                            /region_name="Hydrogen bonded turn"
         Region             120..123
                            /region_name="Helical region"
         Region             124..126
                            /region_name="Hydrogen bonded turn"
         Region             140..141
                            /region_name="Hydrogen bonded turn"
         Region             143..145
                            /region_name="Hydrogen bonded turn"
         Region             147..157
                            /region_name="Beta-strand region"
         Region             159..162
                            /region_name="Hydrogen bonded turn"
         Region             164..165
                            /region_name="Hydrogen bonded turn"
         Region             166..173
                            /region_name="Beta-strand region"
         Region             176
                            /region_name="Beta-strand region"
         Region             182..183
                            /region_name="Hydrogen bonded turn"
         Region             185
                            /region_name="Beta-strand region"
         Region             188..197
                            /region_name="Beta-strand region"
         Region             198..201
                            /region_name="Hydrogen bonded turn"
         Region             202..212
                            /region_name="Beta-strand region"
         Region             215..217
```

```
                             /region_name="Helical region"
          Region            218..219
                             /region_name="Hydrogen bonded turn"
          Region            227..239
                             /region_name="Beta-strand region"
          Region            240..241
                             /region_name="Hydrogen bonded turn"
          Region            242..252
                             /region_name="Beta-strand region"
          Region            264..274
                             /region_name="Beta-strand region"
          Region            280..292
                             /region_name="Beta-strand region"
          Region            294
                             /region_name="Beta-strand region"
          Region            295..297
                             /region_name="Hydrogen bonded turn"
          Region            298
                             /region_name="Beta-strand region"
          Region            301..313
                             /region_name="Beta-strand region"
          Region            318..327
                             /region_name="Beta-strand region"
          Region            334..335
                             /region_name="Hydrogen bonded turn"
          Region            342..350
                             /region_name="Beta-strand region"
          Site              351
                             /site_type="mutagenized"
                             /note="F->Y,N,S,V: LESS RESISTANT TO TR
ORIGIN
          1 mkkstlalvv mgivasasvq aaeiynkdgn kldvygkvka mhymsd
         61 fkgetqindq ltgygrweae fagnkaesdt aqqktrlafa glkykd
        121 dveawtdmfp efggdssaqt dnfmtkrasg latyrntdff gvidgl
        181 vkkqngdgfg tsltydfggs dfaisgaytn sdrtneqnlq srgtgk
        241 niylatfyse trkmtpitgg fanktqnfea vaqyqfdfgl rpslgy
        301 dlvnyidvga tyyfnknmsa fvdykinqld sdnklninnd divavg
//
```

Revised: October 24, 2001.